T150. REAL-TIME FMRI NEUROFEEDBACK TO DOWN-REGULATE SUPERIOR TEMPORAL GYRUS ACTIVITY IN PATIENTS WITH SCHIZOPHRENIA AND AUDITORY HALLUCINATIONS: A PROOF-OF-CONCEPT STUDY

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Background: Neurocognitive models and previous neuroimaging work posit that auditory verbal hallucinations (AVH) arise due to increased auditory cortex (AC) activity and altered connectivity between the AC and other speech and language regions [e.g. 1]. In the present study we examined if patients with schizophrenia (SCZ) and AVH could be trained to down-regulate AC activity using real time functional Magnetic Resonance Imaging neurofeedback (rtfMRI-NF) [2]. We also examined the effects of rtfMRI-NF training on functional connectivity between the AC and other speech and language regions.

Methods: Eleven patients with SCZ (Table 1) and treatment refractory AVH were recruited to participate in the study and were trained to down-regulate auditory cortex (AC) activity over an average of fourteen rtfMRI-NF runs conducted during a two-week training period (Fig 1). We used a functional localiser to identify the speech sensitive superior temporal cortex (STG) (Figure 2A). At the end of the training period, AC activity, functional connectivity and AVH symptom levels were compared pre and post training.

Results: Patients successfully learnt to down-regulate activity in their AC over the rtfMRI-NF training period. Post training, patients showed increased connectivity between the AC, the inferior prefrontal gyrus and the inferior parietal lobe Figure. There was also a modest reduction in AVH symptom levels post compared to pre training (Table 2).

Discussion: The AC is as suitable target region for rtfMRI-NF in patients with SCZ and treatment refractory AVH. Successful down-regulation of AC activity can increase functional connectivity between speech motor and perception regions. These findings raise the possibility that rtfMRI-NF training could be used as a novel therapeutic intervention in this clinical population.

T151. APATHY AND DIMINISHED EXPRESSION ARE NOT ASSOCIATED WITH VENTRAL OR DORSAL STRIATUM VOLUME IN SCHIZOPHRENIA

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Background: Negative symptoms are core features of schizophrenia and can be grouped into two domains. These are apathy including anhedonia, avolition and asociality as well as diminished expression including blunted affect and alogia. A large body of research found that ventral striatal hypo-activation is linked to negative symptoms. In particular, it has been shown that this neural correlate is specific for apathy but not diminished expression. Here, we investigated whether this dissociation can also be found in ventral striatal volume.

Methods: We included brain structural T1 MRI data of 60 patients diagnosed with schizophrenia (SZ) and 58 healthy controls (HC). Negative symptoms in these groups have been assessed using the Brief Negative Symptom Scale (BNSS). We performed voxel-based morphometry (VBM) using the statistical parametric mapping package (SPM 12; Welcome Trust Centre for Neuroimaging, London). We performed a region of interest (ROI) analysis of ventral and dorsal striatal volume between patients with schizophrenia and healthy controls. Furthermore, we analyzed the correlation of right and left ventral striatal volume with apathy and diminished expression in patients with schizophrenia. Moreover, we analyzed potential group differences in gray matter volume in an exploratory whole-brain analysis. Finally, we performed an exploratory whole-brain linear regression to identify potential correlations between the two negative symptom dimensions and gray matter volume. (cluster-defining threshold of p < 0.001, cluster-level pFWE < 0.05)

Results: Patients with schizophrenia showed no differences in ventral striatal volume compared to healthy controls. Apathy or diminished expression did not correlate with ventral or dorsal striatal gray matter volume in patients with schizophrenia. In the exploratory whole-brain analysis we found significant less gray matter volume in the right insula of schizophrenia patients compared to healthy controls (cluster-level pFWE = 0.03, peak (x,y,z) = -46,-15,20). Our exploratory whole-brain linear regression revealed no significant correlation between apathy or diminished expression and gray matter volume changes in patients with schizophrenia.

Discussion: Although a correlation of apathy and ventral striatal volume has been shown in a previous study with fewer subjects, we could not reproduce this finding in a larger group of 60 patients with schizophrenia (Roth et al. 2016). However, while these negative findings do not support the association between apathy and ventral striatal volume, there may be more subtle brain structural changes linked to the pathophysiology of apathy, which cannot be detected by voxel based morphometry. The gray matter reduction in the right insula in subjects with schizophrenia replicated findings from previous studies in schizophrenia (Fornito et al. 2009).

T152. NRN1 GENE AND FUNCTIONAL MRI: ASSOCIATION ANALYSIS IN SCHIZOPHRENIA PATIENTS AND HEALTHY SUBJECTS

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Background: Alterations of synaptic plasticity are currently accepted to play a critical role in schizophrenia (SZ). Among genes of neuronal plasticity there is Neuritin1 gene (NRN1), which has been associated with SZ, age at onset and differences in general cognitive performance in this disorder. However, little is known about the brain imaging correlates of NRN1 gene. We aimed: i) to investigate the association of NRN1 with schizophrenia-spectrum disorders (SZ-SD), exploring its role in age at onset through a family-based study, ii) to examine the brain functional correlates of NRN1 sequence variants through a neuroimaging genetics approach using a case-control design.

Methods: A family-based association analysis was carried out with a sample of 588 individuals from 159 families (74 early onset / 85 adult onset) with an offspring with a diagnosis of SZ-SD. An independent sample consisting of 45 subjects (26 patients / 19 controls) was used to perform a case-control neuroimaging genetics analysis. DNA was extracted from blood/buccal mucosa samples and eleven Single Nucleotide Polymorphisms (SNPs) in NRN1 were genotyped. The linkage disequilibrium between the SNPs was estimated in the family-based sample with Haploviz v4.1.

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